

CLAIMS

What is claimed is:

1. A composition consisting of an isolated polynucleotide comprising a nucleotide sequence encoding a first polypeptide of at least 48 amino acids that has at least 75% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a polypeptide of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22 or an isolated polynucleotide comprising the complement of the nucleotide sequence.
- 5 2. The composition of Claim 1, wherein the isolated nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.
- 10 3. The composition of Claim 1 wherein the isolated polynucleotide is DNA.
4. The composition of Claim 1 wherein the isolated polynucleotide is RNA.
- 15 5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.
6. An isolated host cell comprising the chimeric gene of Claim 5.
7. An isolated host cell comprising an isolated polynucleotide of Claim 1.
8. The isolated host cell of Claim 7 wherein the isolated host selected from the group consisting of yeast, bacteria, plant, and virus.
- 20 9. A virus comprising the isolated polynucleotide of Claim 1.
10. A composition comprising a polypeptide of at least 48 amino acids that has at least 75% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of a polypeptide of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.
- 25 11. A method of selecting an isolated polynucleotide that affects the level of expression of a polypeptide in a plant cell, the method comprising the steps of:
 - (a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 18, 19 and 21 and the complement of such nucleotide sequences;
 - 30 (b) introducing the isolated polynucleotide into a plant cell;
 - (c) measuring the level of a polypeptide in the plant cell containing the polynucleotide; and
 - 35 (d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the isolated polynucleotide.

12. The method of Claim 11 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20 and 22.

5 13. A method of selecting an isolated polynucleotide that affects the level of expression of polypeptide in a plant cell, the method comprising the steps of:

- (a) constructing an isolated polynucleotide of Claim 1;
- (b) introducing the isolated polynucleotide into a plant cell;
- (c) measuring the level of polypeptide in the plant cell containing the polynucleotide; and
- (d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the polynucleotide.

10 14. A method of obtaining a nucleic acid fragment encoding a polypeptide comprising the steps of:

- (a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 40 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 and the complement of such nucleotide sequences; and
- (b) amplifying a nucleic acid sequence using the oligonucleotide primer.

15 15. A method of obtaining a nucleic acid fragment encoding the amino acid sequence encoding a phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase comprising the steps of:

- (a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 and the complement of such nucleotide sequences;
- (b) identifying a DNA clone that hybridizes with the isolated polynucleotide;
- (c) isolating the identified DNA clone; and
- (d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.